OIPE

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/899,732   TIME: 10:39:04

Input Set : A:\57453c1.app
Output Set: N:\CRF3\07242001\I899732.raw

Does Not Comply
Corrected Diskette Needed

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      3 <110> APPLICANT: Salon et al, John A.
      5 <120> TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
      6        Receptor (MCH1) And Uses Thereof
      8 <130> FILE REFERENCE: 1795/57453-C/JPW
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/899,732
     11 <141> CURRENT FILING DATE: 2001-07-05
     13 <150> PRIOR APPLICATION NUMBER: 09/610,635
     14 <151> PRIOR FILING DATE: 2000-07-05
     16 <160> NUMBER OF SEQ ID NOS: 28
     18 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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    375 <210> SEQ ID NO: 16
    376 <211> LENGTH: 100
    377 <212> TYPE: PRT
    378 <213> ORGANISM: Artificial Sequence
    380 <220> FEATURE:
    381 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
E--> 382       MCH1
W--> 384 <210> SEQ ID NO:
W--> 384 <211> LENGTH:
W--> 384 <212> TYPE:
W--> 384 <213> ORGANISM:
    384 <400> SEQUENCE: 16
E--> 385 Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu
    386   1                   5                  10                  15
    388 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
    389               20                  25                  30
    391 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
    392           35                  40                  45
    394 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
    395       50                  55                  60
    397 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
    398 65                  70                  75                  80
    400 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
    401               85                  90                  95
    403 Gly Ser Pro Pro
    404           100
    407 <210> SEQ ID NO: 17
    408 <211> LENGTH: 100
    409 <212> TYPE: PRT
    410 <213> ORGANISM: Artificial Sequence
    412 <220> FEATURE:
    413 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
E--> 414       MCH1
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Input Set : A:\57453c1.app
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W--> 416 <210> SEQ ID NO:
W--> 416 <211> LENGTH:
W--> 416 <212> TYPE:
W--> 416 <213> ORGANISM:
     416 <400> SEQUENCE: 17
E--> 417 Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
     418   1               5                  10                  15
     420 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
     421              20                  25                  30
     423 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
     424              35                  40                  45
     426 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
     427       50                  55                  60
     429 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
     430   65                  70                  75                  80
     432 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
     433              85                  90                  95
     435 Gly Ser Pro Pro
     436             100
     535 <210> SEQ ID NO: 26
     536 <211> LENGTH: 422
     537 <212> TYPE: PRT
     538 <213> ORGANISM: Artificial Sequence
     540 <220> FEATURE:
     541 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
E--> 542      MCH1
W--> 544 <210> SEQ ID NO:
W--> 544 <211> LENGTH:
W--> 544 <212> TYPE:
W--> 544 <213> ORGANISM:
     544 <400> SEQUENCE: 26
E--> 545 Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
     546   1               5                  10                  15
     548 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
     549              20                  25                  30
     551 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
     552              35                  40                  45
     554 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
     555       50                  55                  60
     557 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
     558   65                  70                  75                  80
     560 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
     561              85                  90                  95
     563 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
     564             100                 105                 110
     566 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
     567             115                 120                 125
     569 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
     570             130                 135                 140
```

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572 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
573 145                 150                 155                 160
575 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
576                 165                 170                 175
578 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
579                 180                 185                 190
581 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
582             195             200             205
584 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
585     210                 215                 220
587 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
588 225                 230                 235                 240
590 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
591                 245                 250                 255
593 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
594                 260                 265                 270
596 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
597             275                 280                 285
599 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
600     290                 295                 300
602 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
603 305                 310                 315                 320
605 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
606                 325                 330                 335
608 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
609             340                 345                 350
611 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
612     355                 360                 365
614 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
615     370                 375                 380
617 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
618 385                 390                 395                 400
620 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
621             405                 410                 415
623 Thr Glu Ser Lys Gly Thr
624             420
627 <210> SEQ ID NO: 27
628 <211> LENGTH: 422
629 <212> TYPE: PRT
630 <213> ORGANISM: Artificial Sequence
632 <220> FEATURE:
633 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
634        MCH1
636 <210> SEQ ID NO:
636 <211> LENGTH:
636 <212> TYPE:
636 <213> ORGANISM:
636 <400> SEQUENCE: 27
637 Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
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E--> 634
W--> 636
W--> 636
W--> 636
W--> 636
E--> 637

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/899,732   TIME: 10:39:04

Input Set : A:\57453c1.app
Output Set: N:\CRF3\07242001\I899732.raw

```
638   1             5               10              15
640 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
641           20              25              30
643 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
644           35              40              45
646 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
647      50              55              60
649 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
650 65              70              75              80
652 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
653              85              90              95
655 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
656           100             105             110
658 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
659           115             120             125
661 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
662      130             135             140
664 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
665 145             150             155             160
667 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
668           165             170             175
670 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
671           180             185             190
673 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
674      195             200             205
676 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
677      210             215             220
679 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
680 225             230             235             240
682 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
683           245             250             255
685 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
686           260             265             270
688 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
689      275             280             285
691 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
692      290             295             300
694 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
695 305             310             315             320
697 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
698           325             330             335
700 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
701           340             345             350
703 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
704           355             360             365
706 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
707      370             375             380
709 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
710 385             390             395             400
```

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PATENT APPLICATION: US/09/899,732   TIME: 10:39:04

Input Set : A:\57453c1.app
Output Set: N:\CRF3\07242001\I899732.raw

```
      712 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
      713                 405                 410                 415
      715 Thr Glu Ser Lys Gly Thr
      716                 420
      719 <210> SEQ ID NO: 28
      720 <211> LENGTH: 353
      721 <212> TYPE: PRT
      722 <213> ORGANISM: Artificial Sequence
      724 <220> FEATURE:
      725 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
E--> 726      MCH1
W--> 728 <210> SEQ ID NO:
W--> 728 <211> LENGTH:
W--> 728 <212> TYPE:
W--> 728 <213> ORGANISM:
      728 <400> SEQUENCE: 28
E--> 729 Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn
      730   1               5                 10                  15
      732 Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
      733             20              25                  30
      735 Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
      736             35              40                  45
      738 Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
      739         50                  55                  60
      741 Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
      742   65                  70                  75                  80
      744 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
      745             85                  90                  95
      747 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
      748             100                 105                 110
      750 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
      751             115                 120                 125
      753 Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
      754         130                 135                 140
      756 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
      757 145                 150                 155                 160
      759 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
      760                 165                 170                 175
      762 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
      763             180                 185                 190
      765 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
      766             195                 200                 205
      768 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
      769         210                 215                 220
      771 Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala
      772 225                 230                 235                 240
      774 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
      775                 245                 250                 255
      777 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
```

```
778              260                  265                  270
780 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
781          275                  280                  285
783 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
784      290                  295                  300
786 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
787 305              310                  315                  320
789 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala
790              325                  330                  335
792 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
793          340                  345                  350
795 Thr
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VERIFICATION SUMMARY   DATE: 07/24/2001
PATENT APPLICATION: **US/09/899,732**   TIME: 10:39:05

Input Set : **A:\57453c1.app**
Output Set: **N:\CRF3\07242001\I899732.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:382 M:252 E: No. of Seq. differs, <211>LENGTH:Input:100 Found:0 SEQ:16
L:384 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:414 M:252 E: No. of Seq. differs, <211>LENGTH:Input:100 Found:0 SEQ:17
L:416 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:542 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:0 SEQ:26
L:544 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:634 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:0 SEQ:27
L:636 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:726 M:252 E: No. of Seq. differs, <211>LENGTH:Input:353 Found:0 SEQ:28
L:728 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <213> is required.
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